



SEQUENCE LISTING

<110> de Lencastre, Primal
Nowak, Grzegorz
Pestic-Dragovich, Lidiya
Stojiljkovic, Ljuba
Hozak, Pavel

<120> Nuclear Myosin I B with A 16 Amino Acid N-Terminal Extension

<130> 30151/92399

<140> 09/893,371
<141> 2001-06-27

<150> 60/214,944
<151> 2000-06-29

<160> 8

<170> PatentIn version 3.2

<210> 1
<211> 1044
<212> PRT
<213> Artificial

<220>
<223> Nuclear Myosin 1 beta

<400> 1

Met Arg Tyr Arg Ala Ser Ala Leu Gly Ser Asp Gly Val Arg Val Thr
1 5 10 15

Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val Gln Asp Phe
20 25 30

Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile Glu Asn Leu
35 40 45

Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile Gly Pro Val
50 55 60

Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr Ser Arg Gln
65 70 75 80

His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val Pro Pro His
85 90 95

Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg Thr Glu Arg

100

105

110

Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr
 115 120 125

Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr Cys Pro Ala
 130 135 140

Pro Glu Arg Gly Gly Ala Val Arg Asp Arg Leu Leu Gln Ser Asn Pro
 145 150 155 160

Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn Asp Asn Ser
 165 170 175

Ser Arg Phe Gly Lys Tyr Met Asp Val Gln Phe Asp Phe Lys Gly Ala
 180 185 190

Pro Val Gly Gly His Ile Leu Ser Tyr Leu Leu Glu Lys Ser Arg Val
 195 200 205

Val His Gln Asn His Gly Glu Arg Asn Phe His Val Phe Tyr Gln Leu
 210 215 220

Leu Glu Gly Gly Glu Glu Glu Thr Leu Arg Arg Leu Gly Leu Glu Arg
 225 230 235 240

Asn Pro Gln Ser Tyr Leu Tyr Leu Val Lys Gly Gln Cys Ala Lys Val
 245 250 255

Ser Ser Ile Asn Asp Lys Ser Asp Trp Lys Val Met Arg Lys Ala Leu
 260 265 270

Ser Val Ile Asp Phe Thr Glu Asp Glu Val Glu Asp Leu Leu Ser Ile
 275 280 285

Val Ala Ser Val Leu His Leu Gly Asn Ile His Phe Ala Ala Asp Glu
 290 295 300

Asp Ser Asn Ala Gln Val Thr Thr Glu Asn Gln Leu Lys Tyr Leu Thr
 305 310 315 320

Arg Leu Leu Gly Val Glu Gly Thr Thr Leu Arg Glu Ala Leu Thr His
 325 330 335

Arg Lys Ile Ile Ala Lys Gly Glu Glu Leu Leu Ser Pro Leu Asn Leu
340 345 350

Glu Gln Ala Ala Tyr Ala Arg Asp Ala Leu Ala Lys Ala Val Tyr Ser
355 360 365

Arg Thr Phe Thr Trp Leu Val Arg Lys Ile Asn Arg Ser Leu Ala Ser
370 375 380

Lys Asp Ala Glu Ser Pro Ser Trp Arg Ser Thr Thr Val Leu Gly Leu
385 390 395 400

Leu Asp Ile Tyr Gly Phe Glu Val Phe Gln His Asn Ser Phe Glu Gln
405 410 415

Phe Cys Ile Asn Tyr Cys Asn Glu Lys Leu Gln Gln Leu Phe Ile Glu
420 425 430

Leu Thr Leu Lys Ser Glu Gln Glu Glu Tyr Glu Ala Glu Gly Ile Ala
435 440 445

Trp Glu Pro Val Gln Tyr Phe Asn Asn Lys Ile Ile Cys Asp Leu Val
450 455 460

Glu Glu Lys Phe Lys Gly Ile Ile Ser Ile Leu Asp Glu Glu Cys Leu
465 470 475 480

Arg Pro Gly Glu Ala Thr Asp Leu Thr Phe Leu Glu Lys Leu Glu Asp
485 490 495

Thr Val Lys Pro His Pro His Phe Leu Thr His Lys Leu Ala Asp Gln
500 505 510

Lys Thr Arg Lys Ser Leu Asp Arg Gly Glu Phe Arg Leu Leu His Tyr
515 520 525

Ala Gly Glu Val Thr Tyr Ser Val Thr Gly Phe Leu Asp Lys Asn Asn
530 535 540

Asp Leu Leu Phe Arg Asn Leu Lys Glu Thr Met Cys Ser Ser Met Asn
545 550 555 560

Pro Ile Met Ala Gln Cys Phe Asp Lys Ser Glu Leu Ser Asp Lys Lys
565 570 575

Arg Pro Glu Thr Val Ala Thr Gln Phe Lys Met Ser Leu Leu Gln Leu
580 585 590

Val Glu Ile Leu Arg Ser Lys Glu Pro Ala Tyr Ile Arg Cys Ile Lys
595 600 605

Pro Asn Asp Ala Lys Gln Pro Gly Arg Phe Asp Glu Val Leu Ile Arg
610 615 620

His Gln Val Lys Tyr Leu Gly Leu Met Glu Asn Leu Arg Val Arg Arg
625 630 635 640

Ala Gly Phe Ala Tyr Arg Arg Lys Tyr Glu Ala Phe Leu Gln Arg Tyr
645 650 655

Lys Ser Leu Cys Pro Glu Thr Trp Pro Met Trp Ala Gly Arg Pro Gln
660 665 670

Asp Gly Val Ala Val Leu Val Arg His Leu Gly Tyr Lys Pro Glu Glu
675 680 685

Tyr Lys Met Gly Arg Thr Lys Ile Phe Ile Arg Phe Pro Lys Thr Leu
690 695 700

Phe Ala Thr Glu Asp Ser Leu Glu Val Arg Arg Gln Ser Leu Ala Thr
705 710 715 720

Lys Ile Gln Ala Ala Trp Arg Gly Phe His Trp Arg Gln Lys Phe Leu
725 730 735

Arg Val Lys Arg Ser Ala Ile Cys Ile Gln Ser Trp Trp Arg Gly Thr
740 745 750

Leu Gly Arg Arg Lys Ala Ala Lys Arg Lys Trp Ala Ala Gln Thr Ile
755 760 765

Arg Arg Leu Ile Arg Gly Phe Ile Leu Arg His Ser Pro Arg Cys Pro
770 775 780

Glu	Asn	Ala	Phe	Phe	Leu	Asp	His	Val	Arg	Ala	Ser	Phe	Leu	Leu	Asn	
785					790					795					800	
Leu	Arg	Arg	Gln	Leu	Pro	Arg	Asn	Val	Leu	Asp	Thr	Ser	Trp	Pro	Thr	
				805					810						815	
Pro	Pro	Pro	Ala	Leu	Arg	Glu	Ala	Ser	Glu	Leu	Leu	Arg	Glu	Leu	Cys	
			820					825						830		
Met	Lys	Asn	Met	Val	Trp	Lys	Tyr	Cys	Arg	Ser	Ile	Ser	Pro	Glu	Trp	
		835					840					845				
Lys	Gln	Gln	Leu	Gln	Gln	Lys	Ala	Val	Ala	Ser	Glu	Ile	Phe	Lys	Gly	
	850					855						860				
Lys	Lys	Asp	Asn	Tyr	Pro	Gln	Ser	Val	Pro	Arg	Leu	Phe	Ile	Ser	Thr	
865					870					875					880	
Arg	Leu	Gly	Thr	Glu	Glu	Ile	Ser	Pro	Arg	Val	Leu	Gln	Ser	Leu	Gly	
				885					890						895	
Ser	Glu	Pro	Ile	Gln	Tyr	Ala	Val	Pro	Val	Val	Lys	Tyr	Asp	Arg	Lys	
			900					905						910		
Gly	Tyr	Lys	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu	Thr	Pro	Ser	Ala	Val	
		915					920						925			
Val	Ile	Val	Glu	Asp	Ala	Lys	Val	Lys	Gln	Arg	Ile	Asp	Tyr	Ala	Asn	
	930					935						940				
Leu	Thr	Gly	Ile	Ser	Val	Ser	Ser	Leu	Ser	Asp	Ser	Leu	Phe	Val	Leu	
945					950					955					960	
His	Val	Gln	Arg	Glu	Asp	Asn	Lys	Gln	Lys	Gly	Asp	Val	Val	Leu	Gln	
				965					970						975	
Ser	Asp	His	Val	Ile	Glu	Thr	Leu	Thr	Lys	Thr	Ala	Leu	Ser	Ala	Asp	
			980					985						990		
Arg	Val	Asn	Asn	Ile	Asn	Ile	Asn	Gln	Gly	Ser	Ile	Thr	Phe	Ala	Gly	
		995					1000								1005	
Gly	Pro	Gly	Arg	Asp	Gly	Ile	Ile	Asp	Phe	Thr	Ser	Gly	Ser	Glu		

1010

1015

1020

Leu Leu Ile Thr Lys Ala Lys Asn Gly His Leu Ala Val Val Ala
 1025 1030 1035

Pro Arg Leu Asn Ser Arg
 1040

<210> 2
 <211> 16
 <212> PRT
 <213> Artificial

<220>
 <223> N-terminal 16 amino acid extension

<400> 2

Met Arg Tyr Arg Ala Ser Ala Leu Gly Ser Asp Gly Val Arg Val Thr
 1 5 10 15

<210> 3
 <211> 3661
 <212> DNA
 <213> Artificial

<220>
 <223> NMI Beta

<400> 3
 ggagcggggc gccgggtccg gcaggatgcg ctaccgggca tcggccctgg gcagtgcagg 60
 ggttcgagtg accatggaga ggccttgac tgcccagac cgggtagggg tgcaggactt 120
 tgtcctgctg gagaatttca ccagtgaggc tgccttcatt gagaacctcc ggcggcgggt 180
 ccgggagAAC ctcatTTata cctacatcgg tcctgtccta gtctctgtca atccctaccg 240
 agacctacag atctacagcc ggcagcatat ggaacgctac cgtgggtgtca gtttctatga 300
 agtaccacct catttgtttg cagtggctga cactgtatac cgggcacttc gtactgagcg 360
 tcgggaccag gcagtgatga tttctggaga gagggggca ggcaagacag aggccaccaa 420
 gagactgctc cagttctatg cagagacctg cccagcccct gaacgggggtg gcgcagtgcg 480
 agaccgctg ttgcagagca acccgtgtt agaggccttt gggaatgccA agactctccg 540
 caacgataac tccagccggt ttggaaagta catggatgtg cagtttgact tcaaggggtgc 600
 ccccgTggga ggccacattc tcagttacct cctggaaaag tcccgggtgg tgcacaaaaa 660
 tcacggagag cggaacttcc acgtctttta ccagctactg gaggggggCG aggaggagac 720

tctccgtcgg ctgggcttgg aacggaaccc ccagagctac ttgtacctgg tgaagggcca	780
gtgtgccaag gtctcctcca tcaacgacaa gagtgactgg aaggttatga ggaaggcgct	840
gtccgtcatt gacttcactg aggatgaagt ggaggacttg ctcagcatcg tggccagcgt	900
cctacatctg ggcaacatcc actttgctgc tgacgaggac agcaatgccc aggttactac	960
tgagaaccag ctcaaatac tgaccaggct ccttggtgtg gaaggtaaa cacttaggga	1020
agccctgacc cacaggaaga tcatcgccaa gggggaagag ctctgagcc cactgaacct	1080
tgaacaggcg gcatatgcaa gggatgcgct tgccaaggct gtgtacagcc ggacattcac	1140
ctggctggtc agaaagatca ataggctact ggcctctaag gacgctgaga gcccagctg	1200
gcgaagcacc acggttcttg ggctcctgga catttacggc tttgaagtgt ttcagcataa	1260
cagcttcgag cagttctgca tcaactactg caatgagaag ctgcagcagc tcttcacga	1320
gctgactctc aagtcggagc aggaggaata cgaggctgag ggcacgcgt gggaacctgt	1380
ccagtacttc aacaacaaga tcatctgtga cctggtagag gagaagttca agggcatcat	1440
ctccatcttg gatgaagagt gcctgcgtcc tggggaggcc acggacctga cttttctgga	1500
gaagttggag gacactgtca agccccaccc tcaattcctg acgcacaagc tcgctgacca	1560
gaagaccagg aaatccctag accgagggga gttccgcctt ctgcattatg ctggagagggt	1620
gacctacagt gtgactgggt ttctggataa aaacaatgac ctctcttcc ggaacctgaa	1680
ggagaccatg tgcagctcaa tgaaccccat catggcccag tgctttgaca agagtgaagt	1740
cagtgacaag aagcggccag gacggtggcc acccagttca agatgagcct cctgcagctc	1800
gtggagatcc tgagggtctaa ggagcctgcc tatatccggt gcatcaagcc aaacgacgcc	1860
aagcagccgg gtcgctttga tgagggtgctc atccgacatc aggtgaagta cctgggactg	1920
atggagaatc tgcgctgctg cagagctggc ttgctctatc gtcgcaaata tgaggctttc	1980
ctgcagagggt acaagtcact gtgccagag acatggccca tgtgggcagg acggccccag	2040
gatgggtgtg ccgtgttggc cagacacctc ggctacaagc cagaagagta caaatgggc	2100
aggactaaga tcttcacccg attccccaag acctattttg ccacagagga ctccctggaa	2160
gtccggcggc agagtctagc caccaagatc caggcgccct ggaggggctt tcattggcga	2220
cagaaatttc tccgggtgaa gcgatcagcc atctgtatcc agtcatggtg gcgtggcaca	2280
ctgggcccga ggaaggcagc caagaggaag tgggcagccc agaccatccg tcgactcatc	2340
cgtggcttca ttttgcgcca ttcaccccg tgccctgaga atgccttctt cttggaccac	2400

gtgcgcgcct catttttgct taacctgagg cggcaactgc cccggaatgt tctggacacc 2460
 tcttggecca caccaccacc tgccctgaga gaggcctcag aactgctacg ggaactgtgc 2520
 atgaagaaca tgggtgtgaa gtactgccgg agcatcagcc ctgagtggaa gcagcagctg 2580
 cagcaaaagg cgggtggctag tgaaattttc aagggcaaga aggacaacta cccccagagt 2640
 gtccccagac tcttcattag cacacggctt ggcacagagg agatcagccc cagagtgtct 2700
 caatccttgg gctctgaacc catccagtat gccgtgcccg tggtaaaata cgaccgtaag 2760
 gggtacaagc ctgccccccg gcagctgctg ctcacgcca gtgctgtggt cattgtggag 2820
 gatgctaaag tcaagcagag aattgattat gccaacctaa ccggaatctc tgtcagtagc 2880
 ctgagtata gcctatttgt gcttcacgtg cagcgtgaag acaacaagca gaaggagat 2940
 gtggtgctgc agagtgatca tgtgatcag acactaacca agacggccct cagtgtgac 3000
 cgcgtgaaca atatcaacat caaccaggc agcataacgt ttgcaggggg tccaggcagg 3060
 gacggcatca ttgacttcac atcgggctca gagcttctca tcaccaaggc taagaatggc 3120
 cacctggctg tgggtggccc acggctgaat tctcgggtgat gaaggctgcg gtggaccgct 3180
 cctgactcct gatgcttccc ttagtcccct cctcccctcc gacttacaa aaactcaagc 3240
 ttcaaacag ggatccatgg acaccctcaa aaccacgct gcaaactcct gccttctgct 3300
 cgccccctct tgaggtgatc aggagccagg gagctacccc atgagtgggc caggccgggc 3360
 cacaccaata gaaaagcaga ggctgagca ggccaggcca gccctctgct gatgccaat 3420
 atctaagaca agggaatttt aactgagggtt ttctctgaga ttttttgatg ctttatagga 3480
 aactattttt ttaagaaagc cattttccta ccctaaacac actggatgtg tttttccctg 3540
 cctcgaacag ggcaaggaat gtaactgaaa gactgactgg gctgggctgg aaggtcctct 3600
 tcttgccaa cccttctta ttcccttgct tgccgtgcca tccacctgca ctttttagcc 3660
 a 3661

<210> 4

<211> 20

<212> PRT

<213> Artificial

<220>

<223> NMI Beta Peptide Overlapping Consensus Start Site

<400> 4

Ala Ser Ala Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala
 1 5 10 15

Leu Thr Ala Arg
20

<210> 5
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Myosin I primer

<400> 5
caggaggtaa ctgagaatgt gg

22

<210> 6
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Adapter primer

<400> 6
ccatcctaatacgcactcact atagggc

27

<210> 7
<211> 24
<212> PRT
<213> Artificial

<220>
<223> peptide encoded by 5' region of mouse NMI Beta cdna

<400> 7

Met Arg Tyr Arg Ala Ser Ala Leu Gly Ser Asp Gly Val Arg Val Thr
1 5 10 15

Met Glu Ser Ala Leu Thr Ala Arg
20

<210> 8
<211> 104
<212> DNA
<213> Artificial

<220>
<223> 5' region of mouse NMI Beta cdna

<400> 8

agcggggcgc cgggtccggc aggatgcgt accgggcatc ggccctgggc agtgacgggg 60

ttcgagtgac catggagagc gccttgactg cccgagaccg ggta 104